

We claim:

1. A method for the fermentative production of at least one sulfur-containing fine chemical, which comprises the following steps:
  - a) fermentation of a coryneform bacteria culture producing the desired sulfur-containing fine chemical, the coryneform bacteria expressing at least one heterologous nucleotide sequence which codes for a protein with homoserine O-acetyltransferase (metA) activity;
  - b) concentration of the sulfur-containing fine chemical in the medium or in the bacterial cells, and
  - c) isolation of the sulfur-containing fine chemical.
2. A method as claimed in claim 1, wherein the sulfur-containing fine chemical comprises L-methionine.
3. A method as claimed in either of the preceding claims, wherein the heterologous metA-encoding nucleotide sequence is less than 100% homologous to the metA-encoding sequence from *Corynebacterium glutamicum* ATCC 13032.
4. A method as claimed in claim 3, wherein the metA-encoding sequence is derived from any of the following organisms:

<i>Corynebacterium diptheriae</i>	ATCC 14779
<i>Mycobacterium leprae</i>	ATCC 43910
<i>Mycobacterium tuberculosis</i> CDC1551	ATCC 25584
<i>Chlorobium tepidum</i>	ATCC 49652
<i>Pseudomonas aeruginosa</i>	ATCC 17933
<i>Caulobacter crescentus</i>	ATCC 19089
<i>Neisseria gonorrhoeae</i>	ATCC 53420
<i>Neisseria meningitidis</i>	ATCC 53414
<i>Pseudomonas fluorescens</i>	ATCC 13525
<i>Burkholderia cepacia</i>	ATCC 25416
<i>Nitrosomonas europaea</i>	ATCC 19718
<i>Haemophilus influenzae</i>	ATCC 51907
<i>Halobacterium</i> sp NRC1	ATCC 33170
<i>Thermus thermophilus</i>	ATCC 27634
<i>Deinococcus radiodurans</i>	ATCC 13939
<i>Saccharomyces cerevisiae</i>	ATCC 10751
<i>Schizosaccharomyces pombe</i>	ATCC 24969
<i>Xylella fastidiosa</i>	ATCC 35881
<i>Emericella nidulans</i>	ATCC 36104
<i>Mesorhizobium loti</i>	ATCC 35173
<i>Acremonium crysogenum</i>	ATCC 11550
<i>Pseudomonas putida</i>	ATCC 47054

Staphylococcus aureus	ATCC 35556
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5. A method as claimed in any of the preceding claims, wherein the metA-encoding sequence comprises a coding sequence according to SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43 and 45 or a nucleotide sequence homologous thereto which codes for a protein with metA activity.

6. A method as claimed in any of the preceding claims, wherein the metA-encoding sequence codes for a protein with metA activity, said protein comprising an amino acid sequence according to SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44 and 46 or an amino acid sequence homologous thereto which represents a protein with metA activity.

7. A method as claimed in any of the preceding claims, wherein the coding metA sequence is a DNA or RNA which can be replicated in coryneform bacteria or is stably integrated into the chromosome.

8. A method as claimed in claim 7, wherein

- a) a bacteria strain transformed with a plasmid vector carrying at least one copy of the coding metA sequence under the control of regulatory sequences is used, or
- b) a strain in which the coding metA sequence has been integrated into the bacteria chromosome is used.

9. A method as claimed in any of the preceding claims, wherein the coding metA sequence is overexpressed.

10. A method as claimed in any of the preceding claims, wherein bacteria are fermented in which additionally at least one further gene of the biosynthetic pathway of the desired sulfur-containing fine chemical has been amplified or mutated such that its activity is not influenced by metabolic metabolites.

11. A method as claimed in any of the preceding claims, wherein bacteria are fermented in which at least one metabolic pathway, which reduces the production of the desired sulfur-containing fine chemical, is at least partially switched off.

12. A method as claimed in any of the preceding claims, wherein coryneform bacteria are

fermented in which, at the same time, at least one of the genes selected from among

- a) the gene *lysC*, which encodes an aspartate kinase,
- b) the glyceraldehyde-3-phosphate dehydrogenase-encoding gene *gap*,
- 5 c) the 3-phosphoglycerate kinase-encoding gene *pgk*,
- d) the pyruvate carboxylase-encoding gene *pyc*,
- e) the triose phosphate isomerase-encoding gene *tpi*,
- f) the methylene tetrahydrofolate reductase-encoding gene *metF*,
- g) the cystathionine gamma-synthase-encoding gene *metB*,
- 10 h) the cystathionine gamma-lyase-encoding gene *metC*,
- i) serine hydroxymethyltransferase-encoding gene *glyA*,
- j) the O-acetylhomoserine sulfhydrylase-encoding gene *metY*,
- k) the vitamin B12-dependent methionine synthase-encoding gene *metH*,
- l) the phosphoserine aminotransferase-encoding gene *serC*,
- 15 m) the phosphoserine phosphatase-encoding gene *serB*,
- n) the serine acetyltransferase-encoding gene *cysE*, and
- o) the gene *hom*, which encodes a homoserine dehydrogenase,

is overexpressed or mutated in such a way that the activity of the corresponding proteins  
20 is influenced by metabolic metabolites to a smaller extent, if at all, compared to nonmutated proteins.

13. A method as claimed in any of the preceding claims, wherein coryneform bacteria are  
fermented in which, at the same time, at least one of the genes selected from among

- 25 a) the homoserine kinase-encoding gene *thrB*,
- b) the threonine dehydratase-encoding gene *ilvA*,
- c) the threonine synthase-encoding gene *thrC*,
- d) the meso-diaminopimelate D-dehydrogenase-encoding gene *ddh*,
- e) the phosphoenolpyruvate carboxykinase-encoding gene *pck*,
- 30 f) the glucose-6-phosphate 6-isomerase-encoding gene *pgi*,
- g) the pyruvate oxidase-encoding gene *poxB*,
- h) the dihydrodipicolinate synthase-encoding gene *dapA*,
- i) the dihydrodipicolinate reductase-encoding gene *dapB*; and
- 35 j) the diaminopicolinate decarboxylase-encoding gene,

is attenuated by changing the rate of expression or by introducing a specific mutation.

14. A method as claimed in one or more of the preceding claims, wherein microorganisms of the species *Corynebacterium glutamicum* are used.
- 5 15. A method for producing an L-methionine-containing animal feed additive from fermentation broths, which comprises the following steps:
- a) culturing and fermentation of an L-methionine-producing microorganism in a fermentation medium;
  - b) removal of water from the L-methionine-containing fermentation broth;
  - 10 c) removal of from 0 to 100% by weight of the biomass formed during fermentation; and
  - d) drying of the fermentation broth obtained according to b) and/or c), in order to obtain the animal feed additive in the desired powder or granule form.
- 15 16. A method as claimed in claim 15, wherein microorganisms according to the definition in any of claims 1 to 14 are used.